49321-120.ST25.txt

SEQUENCE LISTING

<110>  Oregon Health & Science University
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       Fruh, Klaus
       King, Jeff
       Jelinek, Laura
       Hirsch, Alec
       DeFilippis, Victor

<120>  METHODS OF TREATMENT AND DIAGNOSIS USING MODULATORS OF
       VIRUS-INDUCED CELLULAR GENE SEQUENCES

<130>  49321-120

<140>  US
<141>  2004-04-15

<150>  US 60/486,694
<151>  2003-07-11

<150>  US 60/533,103
<151>  2003-12-29

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Cys Thr Glu Lys Ile Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser
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Ser His Arg Ala Arg Pro Arg Pro Ala Arg Glu Ala His Arg Pro His
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Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg Asn Ala His Ala Gly
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His Ser Gly Leu Leu His Gly Pro Ala Ser Arg Ser His Arg Ala Arg
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225                 230                 235                 240

Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser His Pro Ala Pro Leu
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Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys Ser Ile Pro Leu Ala
            260                 265                 270

Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys Ala Leu Ala Ala Arg
        275                 280                 285

Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala Pro Pro Arg Arg Thr
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Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro Gln Asp Thr Gly Gln
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ctgcttctga ctcgattaaa aagggagtga gccataactg gcggctgctc tttcgcca      178

atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag      226
Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu
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Leu Tyr Ala Val Arg Ser Glu Arg Lys Leu His Thr Val Gly Asn Leu
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65                  70                  75                  80

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Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr
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Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser
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gag gac aag tgt gag aca gac ttc tat gat gtc acc tgg ttc aag gtc    754
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Leu Asp Ile Val His Met Gln Ala Ala Ala Glu Gly Ser Ser Arg Asp
305             310             315             320

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aca gca cca ggc aaa ggc aaa ttg agg agt ggg tct aac aca ggc ctg        1330
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Asp Tyr Ile Lys Phe Thr Trp Lys Arg Leu Arg Ser His Ser Arg Gln
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aatgatcctt atgatgtcca acaaggaaat agaggacgaa ggcctgtgtg ttgccaggca    1740

ggcacctggg ctttctggaa tccaaaccac agtcttaggg gcttggtagt ttggaaagtt    1800

cttaggcacc atagaagaac agcagatggc ggtgatcagc agagagattg aactttgagg    1860

aggaagcaga atctttgcaa gaaagtcaga cctgtttctt gtaactgggt tcaaaaagaa    1920

aaaaataata aaaataaaag agagagagaa tcagacctgg gtggaactct cctgctcctc    1980

aggaactatg ggagcctcag actcattgta attcaagctt tccgagtcaa gtgattgaca    2040

actgaagaga cacgtggcta gggttccact ggagaattga aaaggactct tgagccctcc    2100

tggaatggag ctgtataact gtgcagagac tttatccatg ccaatagttg ctgtcccctt    2160

ccagggtca ccttgagagg catgacagct gttccacagg ggctatccct tctcagaaaa    2220

cttctcttct gagcctcttt aacagctttc tccagaacca gtgtctgaac caccctggaa    2280

attctgcctt attatttctt actcaaacat gtttagagtg gatagaaaat tatgcagctt    2340

gcacacccat cgtctttaac cccaaatttc ctttggctat taaaaaagtg gtggcaaaag    2400

gcatcctcaa aagaaagaga aatgaaatat ttttgaatgg ttgcacgtta aaaattaaaa    2460

gaaggaatgg gggcagaatg ccatatttt gagggctgta ctaggtttat ctcatttaag    2520

ccccacaaca ccccacagga gggtaatttt ctaactctag tttgcagagg agcaaattga    2580

ggttcagcaa ggtgagagag gtacccaagg tcacatagct agttatgtga gaaagttaga    2640

gtacagatcc tctggggttt tcagcttatt gtagcatatt ttctccgaaa ggcaaaaatg    2700

tgccctttg gccgggcatg gtagctcaag cctataatcc cagcatgttg agaggctgag    2760

gtgggcagat catttgaggc caggagttca agaccagtct ggccaatatg gagaaacctt    2820

gtctctacta aaaacacaaa aattatctgg gcatggtggg gcatgcctgt agtcccactt    2880

acttgggagg ccgaggcacg agaatcgctt gaacccggga ggtggaggtt gccgtgagcc    2940

aagatcacgc cactgcactc cagcctgggc aacagagcaa gactctgtct caaaaaaaaa    3000

aaatacaata ttttaacaat gtgccctctt aagtgtgcac agatacacat acacggtatt    3060

cccaagagtg gtggcagctc aaaatgatat gtttgagtag acgaacagcc gacatggagt    3120

tcccgtgcac ctacggaagg ggacgctttg aaggaaccaa gtgcattttt atctgtgagt    3180

tctgttgtgt ttgtcaaaaa gtcattgtaa tctttcatag ccatacctgg taagcaaaaa    3240

ctagtaaaga cataggaaca tgcagttta cttggtgttt atgttgcaat ctggttgtga    3300
```

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49321-120.ST25.txt

```
tttatatttt aaagcttggt gctaaaccac aatatgtata gcacatggag tgcctgtaca    3360

agctgatgtt ttgtattttg tgttcctctt tgcatgatct gtcaaagtga gatattttta    3420

cctgcctaaa atatgatgtt taaaagcata aaaaaaaaaa aaaaa                     3465
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<210> 6
<211> 1418
<212> DNA
<213> Homo sapiens


<220>
<221> CDS
<222> (110)..(979)

<400> 6
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ggatcggagc acaccggagc aggctcatcg agaaggcgtc tgcgagacc atg gag aac    118
                                                         Met Glu Asn
                                                           1

gga tac acc tat gaa gat tat aag aac act gca gaa tgg ctt ctg tct    166
Gly Tyr Thr Tyr Glu Asp Tyr Lys Asn Thr Ala Glu Trp Leu Leu Ser
  5                  10                  15

cat act aag cac cga cct caa gtt gca ata atc tgt ggt tct gga tta    214
His Thr Lys His Arg Pro Gln Val Ala Ile Ile Cys Gly Ser Gly Leu
 20                  25                  30                  35

gga ggt ctg act gat aaa tta act cag gcc cag atc ttt gac tac agt    262
Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe Asp Tyr Ser
                 40                  45                  50

gaa atc ccc aac ttt cct cga agt aca gtg cca ggt cat gct ggc cga    310
Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His Ala Gly Arg
             55                  60                  65

ctg gtg ttt ggg ttc ctg aat ggc agg gcc tgt gtg atg atg cag ggc    358
Leu Val Phe Gly Phe Leu Asn Gly Arg Ala Cys Val Met Met Gln Gly
         70                  75                  80

agg ttc cac atg tat gaa ggg tac cca ctc tgg aag gtg aca ttc cca    406
Arg Phe His Met Tyr Glu Gly Tyr Pro Leu Trp Lys Val Thr Phe Pro
         85                  90                  95

gtg agg gtt ttc cac ctt ctg ggt gtg gac acc ctg gta gtc acc aat    454
Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val Val Thr Asn
100                 105                 110                 115

gca gca gga ggg ctg aac ccc aag ttt gag gtt gga gat atc atg ctg    502
Ala Ala Gly Gly Leu Asn Pro Lys Phe Glu Val Gly Asp Ile Met Leu
                120                 125                 130

atc cgt gac cat atc aac cta cct ggt ttc agt ggt cag aac cct ctc    550
Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln Asn Pro Leu
            135                 140                 145

aga ggg ccc aat gat gaa agg ttt gga gat cgt ttc cct gcc atg tct    598
Arg Gly Pro Asn Asp Glu Arg Phe Gly Asp Arg Phe Pro Ala Met Ser
        150                 155                 160
```

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49321-120.ST25.txt

```
gat gcc tac gac cgg act atg agg cag agg gct ctc agt acc tgg aaa        646
Asp Ala Tyr Asp Arg Thr Met Arg Gln Arg Ala Leu Ser Thr Trp Lys
        165             170             175

caa atg ggg gag caa cgt gag cta cag gaa ggc acc tat gtg atg gtg        694
Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr Val Met Val
180             185             190             195

gca ggc ccc agc ttt gag act gtg gca gaa tgt cgt gtg ctg cag aag        742
Ala Gly Pro Ser Phe Glu Thr Val Ala Glu Cys Arg Val Leu Gln Lys
            200             205             210

ctg gga gca gac gct gtt ggc atg agt aca gta cca gaa gtt atc gtt        790
Leu Gly Ala Asp Ala Val Gly Met Ser Thr Val Pro Glu Val Ile Val
            215             220             225

gca cgg cac tgt gga ctt cga gtc ttt ggc ttc tca ctc atc act aac        838
Ala Arg His Cys Gly Leu Arg Val Phe Gly Phe Ser Leu Ile Thr Asn
        230             235             240

aag gtc atc atg gat tat gaa agc ctg gag aag gcc aac cat gaa gaa        886
Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn His Glu Glu
        245             250             255

gtc tta gca gct ggc aaa caa gct gca cag aaa ttg gaa cag ttt gtc        934
Val Leu Ala Ala Gly Lys Gln Ala Ala Gln Lys Leu Glu Gln Phe Val
260             265             270             275

tcc att ctt atg gcc agc att cca ctc cct gac aaa gcc agt tga           979
Ser Ile Leu Met Ala Ser Ile Pro Leu Pro Asp Lys Ala Ser
            280             285

cctgccttgg agtcgtctgg catctcccac acaagaccca agtagctgct accttctttg    1039

gccccttgct ggagtcatgt gcctctgtcc ttaggttgta gcagaaagga aaagattcct    1099

gtccttcacc tttcccactt tcttctacca gacccttctg gtgccagatc ctcttctcaa    1159

agctgggatt acaggtgtga gcatagtgag accttggcgc tacaaaataa agctgttctc    1219

attcctgttc tttcttacac aagagctgga gcccgtgccc taccacacat ctgtggagat    1279

gcccaggatt tgactcgggc cttagaactt tgcatagcag ctgctactag ctctttgaga    1339

taatacattc cgaggggctc agttctgcct tatctaaatc accagagacc aaacaaggac    1399

taatccaata cctcttgga                                                  1418
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<210>  7
<211>  289
<212>  PRT
<213>  Homo sapiens

<400>  7

Met Glu Asn Gly Tyr Thr Tyr Glu Asp Tyr Lys Asn Thr Ala Glu Trp
1               5               10              15


Leu Leu Ser His Thr Lys His Arg Pro Gln Val Ala Ile Ile Cys Gly
            20              25              30
```

49321-120.ST25.txt

Ser Gly Leu Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe
        35                  40                  45

Asp Tyr Ser Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His
    50                  55                  60

Ala Gly Arg Leu Val Phe Gly Phe Leu Asn Gly Arg Ala Cys Val Met
65                  70                  75                  80

Met Gln Gly Arg Phe His Met Tyr Glu Gly Tyr Pro Leu Trp Lys Val
                85                  90                  95

Thr Phe Pro Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val
            100                 105                 110

Val Thr Asn Ala Ala Gly Gly Leu Asn Pro Lys Phe Glu Val Gly Asp
            115                 120                 125

Ile Met Leu Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln
    130                 135                 140

Asn Pro Leu Arg Gly Pro Asn Asp Glu Arg Phe Gly Asp Arg Phe Pro
145                 150                 155                 160

Ala Met Ser Asp Ala Tyr Asp Arg Thr Met Arg Gln Arg Ala Leu Ser
                165                 170                 175

Thr Trp Lys Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr
            180                 185                 190

Val Met Val Ala Gly Pro Ser Phe Glu Thr Val Ala Glu Cys Arg Val
            195                 200                 205

Leu Gln Lys Leu Gly Ala Asp Ala Val Gly Met Ser Thr Val Pro Glu
    210                 215                 220

Val Ile Val Ala Arg His Cys Gly Leu Arg Val Phe Gly Phe Ser Leu
225                 230                 235                 240

Ile Thr Asn Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn
                245                 250                 255

His Glu Glu Val Leu Ala Ala Gly Lys Gln Ala Ala Gln Lys Leu Glu
            260                 265                 270

Gln Phe Val Ser Ile Leu Met Ala Ser Ile Pro Leu Pro Asp Lys Ala

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49321-120.ST25.txt
```
        275                    280                    285
```

Ser


<210>   8
<211>   4343
<212>   DNA
<213>   Homo sapiens


<220>
<221>   CDS
<222>   (11)..(1642)

<400>   8
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agatttgata atg ggc tgc att aaa agt aaa gaa aac aaa agt cca gcc        49
            Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala
            1               5                   10

att aaa tac aga cct gaa aat act cca gag cct gtc agt aca agt gtg      97
Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val
    15                  20                  25

agc cat tat gga gca gaa ccc act aca gtg tca cca tgt ccg tca tct     145
Ser His Tyr Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser
30                  35                  40                  45

tca gca aag gga aca gca gtt aat ttc agc agt ctt tcc atg aca cca     193
Ser Ala Lys Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro
                50                  55                  60

ttt gga gga tcc tca ggg gta acg cct ttt gga ggt gca tct tcc tca     241
Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser
                65                  70                  75

ttt tca gtg gtg cca agt tca tat cct gct ggt tta aca ggt ggt gtt     289
Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val
            80                  85                  90

act ata ttt gtg gcc tta tat gat tat gaa gct aga act aca gaa gac     337
Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp
        95                  100                 105

ctt tca ttt aag aag ggt gaa aga ttt caa ata att aac aat acg gaa     385
Leu Ser Phe Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu
110                 115                 120                 125

gga gat tgg tgg gaa gca aga tca atc gct aca gga aag aat ggt tat     433
Gly Asp Trp Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr
                130                 135                 140

atc ccg agc aat tat gta gcg cct gca gat tcc att cag gca gaa gaa     481
Ile Pro Ser Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu
                145                 150                 155

tgg tat ttt ggc aaa atg ggg aga aaa gat gct gaa aga tta ctt ttg     529
Trp Tyr Phe Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu
        160                 165                 170

aat cct gga aat caa cga ggt att ttc tta gta aga gag agt gaa aca     577
Asn Pro Gly Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr
```

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```
Asn Pro Gly Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr
    175             180                 185
```

```
act aaa ggt gct tat tcc ctt tct att cgt gat tgg gat gag ata agg    625
Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg
190             195                 200                 205
```

```
ggt gac aat gtg aaa cac tac aaa att agg aaa ctt gac aat ggt gga    673
Gly Asp Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly
                210             215                 220
```

```
tac tat atc aca acc aga gca caa ttt gat act ctg cag aaa ttg gtg    721
Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val
            225             230                 235
```

```
aaa cac tac aca gaa cat gct gat ggt tta tgc cac aag ttg aca act    769
Lys His Tyr Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr
            240             245                 250
```

```
gtg tgt cca act gtg aaa cct cag act caa ggt cta gca aaa gat gct    817
Val Cys Pro Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala
        255             260             265
```

```
tgg gaa atc cct cga gaa tct ttg cga cta gag gtt aaa cta gga caa    865
Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln
270             275                 280                 285
```

```
gga tgt ttc ggc gaa gtg tgg atg gga aca tgg aat gga acc acg aaa    913
Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys
                290             295                 300
```

```
gta gca atc aaa aca cta aaa cca ggt aca atg atg cca gaa gct ttc    961
Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe
            305             310                 315
```

```
ctt caa gaa gct cag ata atg aaa aaa tta aga cat gat aaa ctt gtt   1009
Leu Gln Glu Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val
            320                 325                 330
```

```
cca cta tat gct gtt gtt tct gaa gaa cca att tac att gtc act gaa   1057
Pro Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu
        335                 340             345
```

```
ttt atg tca aaa gga agc tta tta gat ttc ctt aag gaa gga gat gga   1105
Phe Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly
350                 355                 360                 365
```

```
aag tat ttg aag ctt cca cag ctg gtt gat atg gct gct cag att gct   1153
Lys Tyr Leu Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala
                370                 375                 380
```

```
gat ggt atg gca tat att gaa aga atg aac tat att cac cga gat ctt   1201
Asp Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu
            385                 390                 395
```

```
cgg gct gct aat att ctt gta gga gaa aat ctt gtg tgc aaa ata gca   1249
Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala
    400                 405                 410
```

```
gac ttt ggt tta gca agg tta att gaa gac aat gaa tac aca gca aga   1297
Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg
415                 420                 425
```

49321-120.ST25.txt

```
caa ggt gca aaa ttt cca atc aaa tgg aca gct cct gaa gct gca ctg      1345
Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu
430              435             440             445

tat ggt cgg ttt aca ata aag tct gat gtc tgg tca ttt gga att ctg      1393
Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
                 450             455             460

caa aca gaa cta gta aca aag ggc cga gtg cca tat cca ggt atg gtg      1441
Gln Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val
             465             470             475

aac cgt gaa gta cta gaa caa gtg gag cga gga tac agg atg ccg tgc      1489
Asn Arg Glu Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys
         480             485             490

cct cag ggc tgt cca gaa tcc ctc cat gaa ttg atg aat ctg tgt tgg      1537
Pro Gln Gly Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp
     495             500             505

aag aag gac cct gat gaa aga cca aca ttt gaa tat att cag tcc ttc      1585
Lys Lys Asp Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe
510             515             520             525

ttg gaa gac tac ttc act gct aca gag cca cag tac cag cca gga gaa      1633
Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu
                 530             535             540

aat tta taa ttcaagtagc ctattttata tgcacaaatc tgccaaaata           1682
Asn Leu


taaagaactt gtgtagattt tctacaggaa tcaaaagaag aaaatcttct ttactctgca    1742

tgtttttaat ggtaaactgg aatcccagat atggttgcac aaaaccactt ttttttcccc    1802

aagtattaaa ctctaatgta ccaatgatga atttatcagc gtatttcagg gtccaaacaa    1862

aatagagcta agatactgat gacagtgtgg gtgacagcat ggtaatgaag gacagtgagg    1922

ctcctgctta tttataaatc atttcctttc ttttttttccc caaagtcaga attgctcaaa   1982

gaaaattatt tattgttaca gataaaactt gagagataaa aagctatacc ataataaaat    2042

ctaaaattaa ggaatatcat gggaccaaat aattccattc cagtttttta aagtttcttg    2102

catttattat tctcaaaagt ttttttctaag ttaaacagtc agtatgcaat cttaatatat   2162

gctttctttt gcatggacat gggccaggtt tttcaaaagg aatataaaca ggatctcaaa    2222

cttgattaaa tgttagacca cagaagtgga atttgaaagt ataatgcagt acattaatat    2282

tcatgttcat ggaactgaaa gaataagaac tttttcactt cagtcctttt ctgaagagtt    2342

tgacttagaa taatgaaggt aactagaaag tgagttaatc ttgtatgagg ttgcattgat    2402

ttttttaaggc aatatataat tgaaactact gtccaatcaa aggggaaatg ttttgatctt    2462

tagatagcat gcaaagtaag acccagcatt ttaaaagccc ttttaaaaa ctagacttcg     2522

tactgtgagt attgcttata tgtccttatg gggatgggtg ccacaaatag aaaatatgac    2582

cagatcaggg acttgaatgc acttttgctc atggtgaata tagatgaaca gagaggaaaa    2642
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49321-120.ST25.txt

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tgtatttaaa agaaatacga gaaaagaaaa tgtgaaagtt ttacaagtta gagggatgga      2702

aggtaatgtt taatgttgat gtcatggagt gacagaatgg ctttgctggc actcagagct      2762

cctcacttag ctatattctg agactttgaa gagttataaa gtataactat aaaactaatt      2822

tttcttacac actaaatggg tatttgttca aaataatgaa gttatggctt cacattcatt      2882

gcagtgggat atggttttta tgtaaaacat ttttagaact ccagttttca aatcatgttt      2942

gaatctacat tcactttttt ttgttttctt ttttgagacg gagtctcgct ctgccgccca      3002

ggctggagtg cagtggcgcg atctcggctc actgcaagct ctgcctccca ggttcacacc      3062

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tgaaaagggg acagttttta ccctaaagtg caaaagtgaa acatacaaaa taagactaat      3422

ttttaagagt aactcagtaa tttcaaaata cagatttgaa tagcagcatt agtggtttga      3482

gtgtctagca aaggaaaaat tgatgaataa aatgaaggtc tggtgtatat gttttaaaat      3542

actctcatat agtcacactt taaattaagc cttatattag gcccctctat tttcaggata      3602

taattcttaa ctatcattat ttacctgatt ttaatcatca gattcgaaat tctgtgccat      3662

ggcgtatatg ttcaaattca aaccattttt aaaatgtgaa gatggacttc atgcaagttg      3722

gcagtggttc tggtactaaa aattgtggtt gttttttctg tttacgtaac ctgcttagta      3782

ttgacactct ctaccaagag ggtcttccta agaagagtgc tgtcattatt tcctcttatc      3842

aacaacttgt gacatgagat tttttaaggg ctttatgtga actatgatat tgtaattttt      3902

ctaagcatat tcaaaagggt gacaaaatta cgtttatgta ctaaatctaa tcaggaaagt      3962

aaggcaggaa aagttgatgg tattcattag gttttaactg aatggagcag ttccttatat      4022

aataacaatt gtatagtagg gataaaacac taacttaatg tgtattcatt ttaaattgtt      4082

ctgtattttt aaattgccaa gaaaaacaac tttgtaaatt tggagatatt ttccaacagc      4142

ttttcgtctt cagtgtctta atgtggaagt taacccttac caaaaaagga agttggcaaa      4202

aacagccttc tagcacactt tttaaatga ataatggtag cctaaactta atatttttat      4262

aaagtattgt aatattgttt tgtggataat tgaaataaaa agttctcatt gaatgcacct      4322

attaaaaaaa aaaaaaaaa a                                                 4343
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<210> 9
<211> 543
<212> PRT

49321-120.ST25.txt

&lt;213&gt;  Homo sapiens

&lt;400&gt;  9

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
1               5                   10                  15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
            20              25                  30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
        35              40                  45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
    50              55                  60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
65              70                  75                  80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
                85                  90                  95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
            100                 105                 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
            115                 120                 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
    130                 135                 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
145                 150                 155                 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
                165                 170                 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
            180                 185                 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
        195                 200                 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
    210                 215                 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
225                 230                 235                 240

49321-120.ST25.txt

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
             245                 250                 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
             260                 265                 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
             275                 280                 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
290                 295                 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
305                 310                 315                 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
                325                 330                 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
             340                 345                 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
             355                 360                 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
             370                 375                 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
385                 390                 395                 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
                405                 410                 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
             420                 425                 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
             435                 440                 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
450                 455                 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
465                 470                 475                 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
                485                 490                 495

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```
Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
        500                 505             510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
        515                 520             525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
    530                 535             540
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<212>  DNA
<213>  artificial sequence

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<223>  HMG20B PMO antisense oligomer

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<220>
<223>  HRH1-specific PMO antisense oligo

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<220>
<223>  YES-specific PMO antisense oligo

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<210>  14
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<212>   DNA
<213>   artificial sequence

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<212>   RNA
<213>   Homo sapiens

<400>   16
aacgccuuuu ggaggugcau c                                                21


<210>   17
<211>   4343
<212>   RNA
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uacaguguca ccauguccgu caucuucagc aaagggaaca gcaguuaauu ucagcagucu   180

uuccaugaca ccauuuggag gauccucagg gguaacgccu uuuggaggug caucuuccuc   240

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ggccuuauau gauuaugaag cuagaacuac agaagaccuu ucauuuaaga agggugaaag   360

auuucaaaua auuaacaaua cggaaggaga uugguggaa gcaagaucaa ucgcuacagg    420

aaagaauggu uauaucccga gcaauuaugu agcgccugca gauuccauuc aggcagaaga   480

augguauuuu ggcaaaaugg ggagaaaaga ugcugaaaga uuacuuuga auccuggaaa    540
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ugacaauggu ggauacuaua ucacaaccag agcacaauuu gauacucugc agaaauuggu      720

gaaacacuac acagaacaug cugaugguuu augccacaag uugacaacug uguguccaac      780

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uguuguuucu gaagaaccaa uuuacauugu cacugaauuu augucaaaag gaagcuuauu     1080

agauuuccuu aaggaaggag auggaaagua uuugaagcuu ccacagcugg uugauauggc     1140

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agcaagguua auugaagaca augaauacac agcaagacaa ggugcaaaau uuccaaucaa     1320

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